



十一

1

SEQUENCE LISTING

<110> MUNROE, DONALD G.
KAMBOJ, RAJENDER
PETERS, DIANA
KOOSHESH, FATEMEH
VYAS, TEJAL B.
GUPTA, ASHWANI K.

<120> AN ISOLATED HUMAN EDG-4 RECEPTOR

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<140> 10/084,507
<141> 2002-02-28

<150> 09/222,995
<151> 1998-12-30

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<170> PatentIn Ver. 2.

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primer

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<210> 11
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<210> 13
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<212> DNA
<213> Homo sapiens

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ggagacgacc tcccgccagg tggccctcgcc attcatcgct atcctctgtt ggcgcattgt 180
ggtggaaaac cttctgggtc tcattgcgtt ggcccgaac acgaagttcc actcggaat 240
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caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt gtttgcggc 360
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<211> 364
<212> DNA
<213> Homo sapiens

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gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg cttcgtagc 300
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ggac 364

<210> 15
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<212> DNA
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cggaatgtt cctgtttctg ggcaacctgg ccgcctccga tctactggca ggcgtggctt 300
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tgcccgggaa 369

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 <221> MOD_RES
 <222> (273)
 <223> Leu or Phe

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 Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu His Tyr Asn Tyr Thr Lys
 10 15 20

gag acg ctg gaa acg cag gag acg acc tcc cgc cag gtg gcc tcg gcc 151
 Glu Thr Leu Glu Thr Gln Glu Thr Ser Arg Gln Val Ala Ser Ala
 25 30 35

ttc atc gtc atc ctc tgt tgc gcc att gtg gtg gaa aac ctt ctg gtg 199
 Phe Ile Val Ile Leu Cys Cys Ala Ile Val Val Glu Asn Leu Leu Val
 40 45 50

ctc att gcg gtg gcc cga aac agc aag ttc cac tcg gca atg tac ctg 247
 Leu Ile Ala Val Ala Arg Asn Ser Lys Phe His Ser Ala Met Tyr Leu
 55 60 65 70

ttt ctg ggc aac ctg gcc tcc gat cta ctg gca ggc gtg gcc ttc 295
 Phe Leu Gly Asn Leu Ala Ser Asp Leu Leu Ala Gly Val Ala Phe
 75 80 85

gta gcc aat acc ttg ctc tct ggc tct gtc acg ctg agg ctg acg cct 343
 Val Ala Asn Thr Leu Leu Ser Gly Ser Val Thr Leu Arg Leu Thr Pro
 90 95 100

gtg cag tgg ttt gcc cgg gag ggc tct gcc ttc atc acg ctc tcg gcc 391
 Val Gln Trp Phe Ala Arg Glu Gly Ser Ala Phe Ile Thr Leu Ser Ala
 105 110 115

tct gtc ttc agc ctc ctg gcc atc gcc att gag cgc cac gtg gcc att 439
 Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg His Val Ala Ile
 120 125 130

gcc aag gtc aag ctg tat ggc agc gac aag agc tgc cgc atg ctt ctg 487
 Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys Ser Cys Arg Met Leu Leu
 135 140 145 150

ctc atc ggg gcc tcg tgg ctc atc tcg ctg gtc ctc ggt ggc ctg ccc 535
 Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu Val Leu Gly Gly Leu Pro
 155 160 165

atc ctt ggc tgg aac tgc ctg ggc cac ctc gag gcc tgc tcc act gtc Ile Leu Gly Trp Asn Cys Leu Gly His Leu Glu Ala Cys Ser Thr Val 170 175 180	583
ctg cct ctc tac gcc aag cat tat gtg ctg tgc gtg gtg acc atc ttc Leu Pro Leu Tyr Ala Lys His Tyr Val Leu Cys Val Val Thr Ile Phe 185 190 195	631
tcc atc atc ctg ttg gcc atc gtg gcc ctg tac gtg cgc atc tac tgc Ser Ile Ile Leu Leu Ala Ile Val Ala Leu Tyr Val Arg Ile Tyr Cys 200 205 210	679
gtg gtc cgc tca agc cac gct gac atg gcc gcc ccg cag acg cta gcc Val Val Arg Ser Ser His Ala Asp Met Ala Ala Pro Gln Thr Leu Ala 215 220 225 230	727
ctg ctc aag acg gtc acc atc gtg cta ggc gtc ttt atc gtc tgc tgg Leu Leu Lys Thr Val Thr Ile Val Leu Gly Val Phe Ile Val Cys Trp 235 240 245	775
ctg ccc gcc ttc agc atc ctc ctt ctg gac tat gcc tgt ccc gtc cac Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp Tyr Ala Cys Pro Val His 250 255 260	823
tcc tgc ccg atc ctc tac aaa gcc cac tac ytt ttc gcc gtc tcc acc Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr Xaa Phe Ala Val Ser Thr 265 270 275	871
ctg aat tcc ctg ctc aac ccc gtc atc tac acg tgg cgc agc cgg gac Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr Thr Trp Arg Ser Arg Asp 280 285 290	919
ctg cgg cgg gag gtg ctt cgg ccg ctg cag tgc tgg cgg ccg ggg gtg Leu Arg Arg Glu Val Leu Arg Pro Leu Gln Cys Trp Arg Pro Gly Val 295 300 305 310	967
ggg gtg caa gga cgg agg cgg ggc ggg acc ccg ggc cac cac ctc ctg Gly Val Gln Gly Arg Arg Gly Gly Thr Pro Gly His His Leu Leu 315 320 325	1015
cca ctc cgc agc tcc agc tcc ctg gag agg ggc atg cac atg ccc acg Pro Leu Arg Ser Ser Ser Leu Glu Arg Gly Met His Met Pro Thr 330 335 340	1063
tca ccc acg ttt ctg gag ggc aac acg gtg gtc tgagggtggg ggtggaccaa 1116 Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val 345 350	
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<221> MOD_RES

<222> (273)

<223> Leu or Phe

<400> 17

Met	Gly	Ser	Leu	Tyr	Ser	Glu	Tyr	Leu	Asn	Pro	Asn	Lys	Val	Gln	Glu
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His	Tyr	Asn	Tyr	Thr	Lys	Glu	Thr	Leu	Glu	Thr	Gln	Glu	Thr	Thr	Ser
						20			25			30			

Arg	Gln	Val	Ala	Ser	Ala	Phe	Ile	Val	Ile	Leu	Cys	Cys	Ala	Ile	Val
						35			40			45			

Val	Glu	Asn	Leu	Leu	Val	Leu	Ile	Ala	Val	Ala	Arg	Asn	Ser	Lys	Phe
						50			55		60				

His	Ser	Ala	Met	Tyr	Leu	Phe	Leu	Gly	Asn	Leu	Ala	Ala	Ser	Asp	Leu
						65			70		75			80	

Leu	Ala	Gly	Val	Ala	Phe	Val	Ala	Asn	Thr	Leu	Leu	Ser	Gly	Ser	Val
						85			90			95			

Thr	Leu	Arg	Leu	Thr	Pro	Val	Gln	Trp	Phe	Ala	Arg	Glu	Gly	Ser	Ala
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Phe	Ile	Thr	Leu	Ser	Ala	Ser	Val	Phe	Ser	Leu	Leu	Ala	Ile	Ala	Ile
						115			120			125			

Glu	Arg	His	Val	Ala	Ile	Ala	Lys	Val	Lys	Leu	Tyr	Gly	Ser	Asp	Lys
						130			135			140			

Ser	Cys	Arg	Met	Leu	Leu	Leu	Ile	Gly	Ala	Ser	Trp	Leu	Ile	Ser	Leu
						145			150		155			160	

Val	Leu	Gly	Gly	Leu	Pro	Ile	Leu	Gly	Trp	Asn	Cys	Leu	Gly	His	Leu
						165			170			175			

Glu	Ala	Cys	Ser	Thr	Val	Leu	Pro	Leu	Tyr	Ala	Lys	His	Tyr	Val	Leu
						180			185			190			

Cys	Val	Val	Thr	Ile	Phe	Ser	Ile	Ile	Leu	Leu	Ala	Ile	Val	Ala	Leu
						195			200			205			

Tyr	Val	Arg	Ile	Tyr	Cys	Val	Val	Arg	Ser	Ser	His	Ala	Asp	Met	Ala
						210			215			220			

Ala	Pro	Gln	Thr	Leu	Ala	Leu	Leu	Lys	Thr	Val	Thr	Ile	Val	Leu	Gly
						225			230			235			240

Val	Phe	Ile	Val	Cys	Trp	Leu	Pro	Ala	Phe	Ser	Ile	Leu	Leu	Asp	
						245			250			255			

Tyr	Ala	Cys	Pro	Val	His	Ser	Cys	Pro	Ile	Leu	Tyr	Lys	Ala	His	Tyr
						260			265			270			

Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285

Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
 290 295 300

Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Thr
 305 310 315 320

Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
 325 330 335

Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
 340 345 350

Val

<210> 18

<400> 18
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<210> 19

<211> 1062

<212> DNA

<213> Homo sapiens

<400> 19

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 aacagcaagt tccactcggc aatgtacctg tttctggca acctggccgc ctccgatcta 240
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<210> 21

<211> 352

<212> PRT

<213> Rattus sp.

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 Arg Lys Val Ala Ser Ala Phe Ile Ile Ile Leu Cys Cys Ala Ile Val
 35 40 45
 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
 50 55 60
 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
 65 70 75 80
 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Pro Val
 85 90 95
 Thr Leu Ser Leu Thr Pro Leu Gln Trp Phe Ala Arg Glu Gly Ser Ala
 100 105 110
 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
 115 120 125
 Glu Arg Gln Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
 130 135 140
 Ser Cys Arg Met Leu Met Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
 145 150 155 160
 Ile Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Asp His Leu
 165 170 175
 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
 180 185 190
 Cys Val Val Thr Ile Phe Ser Val Ile Leu Leu Ala Ile Val Ala Leu
 195 200 205
 Tyr Val Arg Ile Tyr Phe Val Val Arg Ser Ser His Ala Asp Val Ala
 210 215 220
 Gly Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
 225 230 235 240
 Val Phe Ile Ile Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Asp
 245 250 255
 Ser Thr Cys Pro Val Arg Ala Cys Pro Val Leu Tyr Lys Ala His Tyr
 260 265 270
 Phe Phe Ala Phe Ala Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285
 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Leu
 290 295 300

Cys Trp Arg Gln Gly Lys Gly Ala Thr Gly Arg Arg Gly Gly Asn Pro
 305 310 315 320

Gly His Arg Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg Gly
 325 330 335

Leu His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val
 340 345 350

<210> 22

<211> 353

<212> PRT

<213> Homo sapiens

<400> 22

Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
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His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
 20 25 30

Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
 35 40 45

Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
 50 55 60

His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
 65 70 75 80

Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
 85 90 95

Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
 100 105 110

Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
 115 120 125

Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
 130 135 140

Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
 145 150 155 160

Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
 165 170 175

Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
 180 185 190

Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Val Val Ala Leu
 195 200 205

Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
 210 215 220

Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
 225 230 235 240

Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
 245 250 255

Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
 260 265 270

Leu Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285

Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
 290 295 300

Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr
 305 310 315 320

Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
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Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
 340 345 350

Val

<210> 23

<211> 351

<212> PRT

<213> Homo sapiens

<400> 23

Met Val Ile Met Gly Gln Cys Tyr Tyr Asn Glu Thr Ile Gly Phe Phe
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Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
 20 25 30

Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
 35 40 45

Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
 50 55 60

Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
 65 70 75 80

Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
 85 90 95

Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
 100 105 110

Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
 115 120 125

Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
 130 135 140

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
 145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
 165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
 180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
 195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
 210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
 225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
 245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
 260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
 275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
 290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
 305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
 325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Asp Ser Thr Leu
 340 345 350

<210> 24
 <211> 1056
 <212> DNA
 <213> Homo sapiens

<400> 24

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 cggcgcttcc accagcccat ctactacctg ctcggcaatc tggccgcggc tgacctctc 240
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ttcctgctca tggggctgt gtacacccgc atttcttct acgtgcggcg gcgagtgcag 660
cgcatggcag agcatgtcag ctgccacccc cgctaccgag agaccacgct cagcctggc 720
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